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 enhanced for more flexible patent number searching  
 NEWS 26 AUG 27 CAS definition of basic patents expanded to ensure  
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 information

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,  
 AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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=> s c myc  
 L1 43807 C MYC

=> s mRNA (3a) instabi?  
 L2 964 MRNA (3A) INSTABI?

=> s l1 and l2  
L3 29 L1 AND L2

=> dup rem l3  
PROCESSING COMPLETED FOR L3  
L4 15 DUP REM L3 (14 DUPLICATES REMOVED)

=> d bib abs 1-  
YOU HAVE REQUESTED DATA FROM 15 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN  
AN 2004:999715 CAPLUS  
DN 141:406751  
TI Assay and expression systems comprising reporter gene and  
instability  
sequence DNA for identifying compounds which affect stability of  
mRNA  
IN Kastelic, Tania; Cheneval, Dominique  
PA Novation Pharmaceuticals Inc., Can.  
SO U.S. Pat. Appl. Publ., 49 pp., Cont.-in-part of U.S. Ser. No.  
869,159.  
CODEN: USXXCO  
DT Patent  
LA English  
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.
DATE			
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PI US 20040231007	A1	20041118	US 2004-814634
20040401			
WO 2000039314	A1	20000706	WO 1999-CA1235
19991223			
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN,			
CR, CU,			
CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,			
ID, IL,			
IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,			
LV, MA,			
MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,			
SG, SI,			
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA,			
ZW			
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,			
CY, DE,			
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF,			
BJ, CF,			
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 2005229165	A1	20051013	AU 2005-229165
20050401			
CA 2603585	A1	20051013	CA 2005-2603585
20050401			

WO 2005095615                      A1            20051013            WO 2005-CA491

20050401

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1774000                      A1            20070418            EP 2005-730094

20050401

R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR

JP 2007530058                      T            20071101            JP 2007-505349

20050401

US 20070190532                      A1            20070816            US 2007-594851

20070504

PRAI GB 1998-28709                      A            19981224

WO 1999-CA1235                      W            19991223

US 2001-869159                      A2            20010815

US 2004-814634                      A            20040401

WO 2005-CA491                      W            20050401

AB The present invention relates to an assay for the identification of biol. active compds., in particular to a reporter gene assay for the identification of compds., which have an effect on mRNA stability. More particularly, the present invention relates to a reporter gene expression system and cell lines comprising said expression system. The invention further relates to compds. which destabilize mRNA. Radicicol and radicicol analog A showed a clear effect on mRNA stability. Human APP, Bcl-2 $\alpha$ , c-myc, TNF $\alpha$ , IL-1 $\beta$ , VEGF instability sequence were constructed. Instability sequence DNA is from

The gene encoding a cytokine, a gene encoding a chemokine, a gene encoding a nuclear transcription factor, a gene encoding an oxygenase, a proto-oncogene, an immediate early gene, a cell cycle controlling gene, and a gene involved in apoptosis.

L4 ANSWER 2 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN  
DUPLICATE 1

AN 2004:95192 BIOSIS

DN PREV200400084197

TI Mammary tumor induction in transgenic mice expressing an RNA-binding protein.

AU Tessier, Charles R.; Doyle, Glenn A.; Clark, Brad A.; Pitot, Henry C.;

Ross, Jeff [Reprint Author]

CS McArdle Laboratory for Cancer Research, University of Wisconsin-Madison,  
1400 University Avenue, Madison, WI, 53706, USA  
ross@oncology.wisc.edu

SO Cancer Research, (January 1 2004) Vol. 64, No. 1, pp. 209-214.  
print.

ISSN: 0008-5472 (ISSN print).

DT Article

LA English

ED Entered STN: 11 Feb 2004

Last Updated on STN: 11 Feb 2004

AB We have analyzed mammary tumors arising in transgenic mice expressing a

novel, multifunctional RNA-binding protein. The protein, which we call

the c-myc mRNA coding region

instability determinant binding protein (CRD-BP), binds to

c-myc, insulin-like growth factor II, and beta-actin

mRNAs, and to H19 RNA. Depending on the RNA substrate, the

CRD-BP affects

RNA localization, translation, or stability. CRD-BP levels are high

during fetal development but low or undetectable in normal adult tissues.

The CRD-BP is linked to tumorigenesis, because its expression is reactivated in some adult human breast, colon, and lung tumors.

These

data suggest the CRD-BP is a proto-oncogene. To test this idea, the

CRD-BP was expressed from the whey acidic protein (WAP) promoter in

mammary epithelial cells of adult transgenic mice. The incidence of

mammary tumors was 95% and 60% in two lines of WAP-CRD-BP mice with high

and low relative CRD-BP expression, respectively. Some of the tumors metastasized. Nontransgenic mice did not develop mammary tumors. H19 RNA and insulin-like growth factor II mRNA were up-regulated significantly in non-neoplastic WAP-CRD-BP mammary tissue. WAP-CRD-BP mice are a novel model for mammary neoplasia and might provide insights into human breast cancer biology.

L4 ANSWER 3 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN  
DUPLICATE 2

AN 2003:399109 BIOSIS

DN PREV200300399109

TI CRD-BP: A c-myc mRNA stabilizing protein with an oncofetal pattern of expression.

AU Ioannidis, P. [Reprint Author]; Mahaira, L.; Papadopoulou, A.; Teixeira,

M. R.; Heim, S.; Andersen, J. A.; Evangelou, E.; Dafni, U.; Pandis, N.;

Trangas, T.

CS Immunology Center, St Savvas Hospital, 171 Alexandras Ave, Athens, 11522, Greece

pioannidis@ath.forthnet.gr

SO Anticancer Research, (May-June 2003) Vol. 23, No. 3A, pp. 2179-2184.

print.

CODEN: ANTRD4. ISSN: 0250-7005.

DT Article

General Review; (Literature Review)

LA English

ED Entered STN: 27 Aug 2003

Last Updated on STN: 27 Aug 2003

AB The Coding Region Determinant-Binding Protein (CRD-BP) is an RRM and

least three KH-domain-containing protein that recognizes specifically at

least three RNAs. It binds to one of the two c-myc mRNA instability elements, to the 5' Un Translated Region (UTR) of the leader 3 IGF-II mRNA and to the oncofetal H19 RNA. CRD-BP has been

assigned a role in stabilizing c-myc mRNA by preventing its endonucleolytic cleavage and in repressing the translation

of the leader 3 IGF-II mRNA, the major embryonic species of this message.

CRD-BP is normally expressed only in fetal tissues. However, its expression is detected in primary tumors and transformed cell lines of

different origins. The vast majority of colon (80%) and breast (60%) tumors and sarcomas (73%) express CRD-BP whereas in other tumor types, for example prostate carcinomas, its expression is rare. CRD-BP expression has also been detected in benign tumors such as breast fibroadenomas, meningiomas and other benign mesenchymal tumors, implying a role for this gene in abnormal cell proliferation. In breast carcinomas, CRD-BP expression and or gene copy number gains in the region encompassing the c-myc locus were detected in approximately 75% of tumors, implying that the deregulated expression of c-myc may be more widespread than previously believed. Infiltrated lymph nodes, corresponding to CRD-BP- positive primary tumors, were also found positive indicating that monitoring for CRD-BP could prove useful for the detection and monitoring of disseminated disease.

L4 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN

AN 2002:430571 CAPLUS

DN 137:151401

TI Regulation of c-myc mRNA decay by translational pausing in a coding region instability determinant

AU Lemm, Ira; Ross, Jeff

CS McArdle Laboratory for Cancer Research, University of Wisconsin-Madison, Madison, WI, 53706, USA

SO Molecular and Cellular Biology (2002), 22(12), 3959-3969  
CODEN: MCEBD4; ISSN: 0270-7306

PB American Society for Microbiology

DT Journal

LA English

AB A 249-nucleotide coding region instability determinant (CRD) destabilizes

c-myc mRNA. Previous expts. identified a CRD-binding protein (CRD-BP) that appears to protect the CRD from endonuclease

cleavage. However, it was unclear why a CRD-BP is required to protect a

well-translated mRNA whose coding region is covered with ribosomes. We

hypothesized that translational pausing in the CRD generates a ribosome-deficient region downstream of the pause site, and this region is

exposed to endonuclease attack unless it is shielded by the CRD-BP.

Transfection and cell-free translation expts. reported here support this

hypothesis. Ribosome pausing occurs within the c-myc CRD in tRNA-depleted reticulocyte translation reactions. The pause sites map to a rare arginine (CGA) codon and to an adjacent threonine (ACA) codon. Changing these codons to more common codons increases translational efficiency in vitro and increases mRNA abundance in transfected cells. These data suggest that c-myc mRNA is rapidly degraded unless it is (i) translated without pausing or (ii) protected by the CRD-BP when pausing occurs. Addnl. mapping expts. suggest that the CRD is bipartite, with several upstream translation pause sites and a downstream endonuclease cleavage site.

RE.CNT 65        THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD  
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4    ANSWER 5 OF 15   BIOSIS   COPYRIGHT (c) 2008 The Thomson Corporation on STN

AN    2002:308512   BIOSIS

DN    PREV200200308512

TI    Correlation between intrinsic mRNA stability and the affinity of AUFL

(hnRNP D) and HuR for A+U-rich mRNAs.

AU    Blaxall, Burns C.; Pende, Aldo; Wu, Steven C.; Port, J. David  
[Reprint author]

CS    Division of Cardiology, University of Colorado HSC, 4200 East Ninth

Avenue, B139, Denver, CO, 80262, USA  
david.port@uchsc.edu

SO    Molecular and Cellular Biochemistry, (March, 2002) Vol. 232, No. 1-2, pp. 1-11. print.

CODEN: MCBIB8. ISSN: 0300-8177.

DT    Article

LA    English

ED    Entered STN: 22 May 2002

Last Updated on STN: 22 May 2002

AB    Presence of A+U-rich elements (AREs) within 3'-untranslated regions

(3'UTRs) of numerous mRNAs has been associated with rapid mRNA turnover;

however, the interaction of specific factors with AREs is also associated

with mRNA stabilization. Recently, two ARE binding proteins with putative

mRNA destabilizing (AUFL) and stabilizing (HuR) properties have been

described. However, no direct comparison of AUFL and HuR binding properties has been made. Therefore, we examined the relative affinities

of p37AUF1 and HuR for a diverse set of ARE-containing mRNAs encoding beta-adrenergic receptors, a proto-oncogene, and a cytokine. We find that high-affinity AUF1 binding appears to require elements beyond primary nucleotide sequence. In contrast, binding of HuR appears considerably less constrained. As a functional correlate, we determined the ability of these specific mRNA sequences to affect the stability of chimeric beta-globin mRNA constructs. Although the relative affinity of AUF1 and HuR are generally predictive of mRNA stability, we find that certain mRNA sequences do not conform to these generalizations.

L4 ANSWER 6 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN

DUPLICATE 3

AN 2001:313891 BIOSIS

DN PREV200100313891

TI mRNA localization by a 145-nucleotide region of the c-fos 3'-untranslated

region: Links to translation but not stability.

AU Dalglish, Gillian; Veyrune, Jean-Luc; Blanchard, Jean-Marie; Hesketh,

John [Reprint author]

CS Rowett Research Institute, Bucksburn, Aberdeen, AB21 9SB, UK  
j.e.hesketh@ncl.ac.uk

SO Journal of Biological Chemistry, (April 27, 2001) Vol. 276, No. 17, pp.

13593-13599. print.

CODEN: JBCHA3. ISSN: 0021-9258.

DT Article

LA English

ED Entered STN: 4 Jul 2001

Last Updated on STN: 19 Feb 2002

AB The presence of a localization signal in the 3'-untranslated region of

c-fos mRNA was investigated by in situ hybridization and cell fractionation techniques. Cells were transfected with chimeric gene

constructs in which the beta-globin coding region was used as a reporter

and linked to either its own 3'-untranslated region, the c-fos 3'-untranslated region, or the c-fos 3'-untranslated region containing

different deletions. Replacement of the endogenous beta-globin 3'-untranslated region by that from c-fos caused a redistribution of the

transcripts so that they were recovered in cytoskeletal-bound polysomes



and seen localized in the perinuclear cytoplasm. Deletion of the AU-rich instability region did not affect transcript localization, but removal of a distinct 145-nucleotide region of the 3'-untranslated region abolished it. The prevention of transcript translation by desferrioxamine led to a marked loss of transcript localization, independent of mRNA instability. The data show that the 3'-untranslated region of c-fos mRNA, as c-myc, contains a localization signal, which targets the mRNA to the perinuclear cytoskeleton. We propose that this is important to ensure efficient nuclear import of these key regulatory proteins. mRNA localization by the fos 3'-untranslated region is independent of mRNA instability, and the two are determined by different regulatory elements.

L4 ANSWER 7 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN  
DUPLICATE 4

AN 1997:226015 BIOSIS  
DN PREV199799517731

TI Identification of two proteins that bind to a pyrimidine-rich sequence in the 3'-untranslated region of GAP-43 mRNA.

AU Irwin, Nina [Reprint author]; Baekelandt, Veerle; Goritchenko, Lyda; Benowitz, Larry I.

CS Lab. Neurosci. Res. Neurosurg., Children's Hosp., En 308, 300 Longwood Ave., Boston, MA 02115, USA

SO Nucleic Acids Research, (1997) Vol. 25, No. 6, pp. 1281-1288. CODEN: NARHAD. ISSN: 0305-1048.

DT Article

LA English

ED Entered STN: 22 May 1997

Last Updated on STN: 22 May 1997

AB GAP-43 is a membrane phosphoprotein that is important for the development and plasticity of neural connections. In undifferentiated PC12 pheochromocytoma cells, GAP-43 mRNA degrades rapidly ( $t_{1/2}$  = 5 h), but becomes stable when cells are treated with nerve growth factor. To identify trans-acting factors that may influence mRNA stability, we combined column chromatography and gel mobility shift assays to isolate GAP-43 mRNA binding proteins from neonatal bovine brain tissue. This

resulted in the isolation of two proteins that bind specifically and competitively to a pyrimidine-rich sequence in the 3'-untranslated region of GAP-43 mRNA. Partial amino acid sequencing revealed that one of the RNA binding proteins coincides with FBP (far upstream element binding protein), previously characterized as a protein that resembles hnRNP K and which binds to a single-stranded, pyrimidine-rich DNA sequence upstream of the c-myc gene to activate its expression. The other binding protein shares sequence homology with PTB, a polypyrimidine tract binding protein implicated in RNA splicing and regulation of translation initiation. The two proteins bind to a 26 nt pyrimidine-rich sequence lying 300 nt downstream of the end of the coding region, in an area shown by others to confer instability on a reporter mRNA in transient transfection assays. We therefore propose that FBP and the PTB-like protein may compete for binding at the same site to influence the stability of GAP-43 mRNA.

L4 ANSWER 8 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN

DUPLICATE 5

AN 1996:364403 BIOSIS

DN PREV199699086759

TI Identification of sequences in c-myc mRNA that regulate its steady-state levels.

AU Yeilding, Newman M.; Rehman, Muhammad T.; Lee, William M. F.  
[Reprint author]

CS 663 CRB, 415 Curie Blvd., Univ. Pennsylvania, Philadelphia, PA 19104, USA

SO Molecular and Cellular Biology, (1996) Vol. 16, No. 7, pp. 3511-3522.

CODEN: MCEBD4. ISSN: 0270-7306.

DT Article

LA English

ED Entered STN: 14 Aug 1996

Last Updated on STN: 14 Aug 1996

AB The level of cellular myc proto-oncogene expression is rapidly regulated

in response to environmental signals and influences cell proliferation and

differentiation. Regulation is dependent on the fast turnover of

c-myc mRNA, which enables cells to rapidly alter c-myc mRNA levels. Efforts to identify elements in myc mRNA responsible for its instability have used a variety of approaches, all of which require manipulations that perturb normal cell metabolism. These various approaches have implicated different regions of the mRNA and have led to a lack of consensus over which regions actually dictate rapid turnover and low steady-state levels of c-myc mRNA. To identify these regions by an approach that does not perturb cell metabolism acutely and that directly assesses the effect of a c-myc mRNA region on the steady-state levels of c-myc mRNA, we developed an assay using reverse transcription and PCR to compare the steady-state levels of human myc mRNAs transcribed from two similarly constructed myc genes transiently cotransfected into proliferating C2C12 myoblasts. Deletion mutations were introduced into myc genes, and the levels of their mRNAs were compared with that of a near-normal, reference myc mRNA. Deletion of most of the myc 3' untranslated region (UTR) raised myc mRNA levels, while deletion of sequences in the myc 5' UTR (most of exon 1), exon 2, or the protein-coding region of exon 3 did not, thus demonstrating that the 3' UTR is responsible for keeping myc mRNA levels low. Using a similar reverse transcription-PCR assay for comparing the steady-state levels of two beta-globin-myc fusion mRNAs, we showed that fusion of the myc 3' UTR lowers globin mRNA levels by destabilizing beta-globin mRNA. Surprisingly, fusion of the protein-coding region of myc exon 3 also lowered globin mRNA steady-state levels. Investigating the possibility that exon 3 coding sequences may play some other role in regulating c-myc mRNA turnover, we demonstrated that these sequences, but not myc 3' UTR sequences, are necessary for the normal posttranscriptional downregulation of c-myc mRNA during myoblast differentiation. We conclude that, while two elements within c-myc mRNA can act as instability determinants in a heterologous context, only the instability element in the 3' UTR regulates its steady-state levels in

proliferating C2C12 cells.

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AN 1995141433 EMBASE

TI Expression of the blood-clotting factor-VIII cDNA is repressed by a

transcriptional silencer located in its coding region.

AU Hoeben, Rob C., Dr. (correspondence)

CS Lab. of Molecular Carcinogenesis, Department of Medical Biochemistry,

Sylvius Laboratory, Wassenaarseweg 72, 2333 AL Leiden, Netherlands.

AU Fallaux, Frits J.; Cramer, Steve J.; Van Den Wollenberg, Diana J.M.; Van

Ormondt, Hans; Briet, Ernest; Van Der Eb, Alex J.

SO Blood, (1 May 1995) Vol. 85, No. 9, pp. 2447-2454.

Refs: 39

ISSN: 0006-4971 CODEN: BLOOAW

CY United States

DT Journal; Article

FS 022 Human Genetics

025 Hematology

005 General Pathology and Pathological Anatomy

LA English

SL English

ED Entered STN: 31 May 1995

Last Updated on STN: 31 May 1995

AB Hemophilia A is caused by a deficiency of factor-VIII procoagulant (fVIII)

activity. The current treatment by frequent infusions of plasma-derived

fVIII concentrates is very effective but has the risk of transmittance of

blood-borne viruses (human immunodeficiency virus [H/V], hepatitis

viruses). Use of recombinant DNA-derived fVIII as well as gene therapy

could make hemophilia treatment independent of blood-derived products. So

far, the problematic production of the fVIII protein and the low titers of

the fVIII retrovirus stocks have prevented preclinical trials of gene

therapy for hemophilia A in large-animal models. We have initiated a

study of the mechanisms that oppose efficient fVIII synthesis. We have

established that fVIII cDNA contains sequences that dominantly inhibit its

own expression from retroviral as well as from plasmid vectors. The

inhibition is not caused by instability of the fVIII mRNA ( $t(1/2)$ ,  $\pm 6$  hours) but rather to repression at the level of transcription. A 305-bp fragment is identified that is involved in but not sufficient for repression. This fragment does not overlap the region recently identified by Lynch et al (Hum Gene Ther 4:259, 1993) as a dominant inhibitor of RNA accumulation. The repression is mediated by a cellular factor (or factors) and is independent of the orientation of the element in the transcription unit, giving the repressor element the hallmarks of a transcriptional silencer.

L4 ANSWER 10 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on

STN

DUPLICATE 6

AN 1993:209797 BIOSIS

DN PREV199395111022

TI 1,25-Dihydroxyvitamin D-3 destabilizes c-myc mRNA in HL-60 leukemic cells.

AU Mangasarian, Karen; Mellon, William S. [Reprint author]

CS University Wisconsin, School Pharmacy, 425 N. Charter St., Madison, WI 53706, USA

SO Biochimica et Biophysica Acta, (1993) Vol. 1172, No. 1-2, pp. 55-63.

CODEN: BBACAQ. ISSN: 0006-3002.

DT Article

LA English

ED Entered STN: 23 Apr 1993

Last Updated on STN: 23 Apr 1993

AB The differentiation process is accompanied by alterations in the expression of a variety of genes. Monocytic maturation of hematopoietic

cells (HL-60) induced by 1,25-dihydroxyvitamin D-3 (1,25(OH)-2D-3),

results in a decrease in steady state c-myc mRNA levels. To elucidate the mechanism by which 1,25(OH)-2D-3 regulates

c-myc mRNA expression, transcriptional and post-transcriptional modes of regulation were investigated. No transcriptional regulation was identified, however, 1,25(OH)-2D-3 appeared

to decrease steady state c-myc mRNA levels by increasing its turnover rate. Using actinomycin D to block transcription,

the half-life of c-myc mRNA was shown to decrease from 20 min in the absence of 1,25(OH)-2D-3 to 15 min in the presence of

1,25(OH)-2D-3. Cycloheximide reversed the instability induced by 1,25(OH)-2D-3, prolonging the half-life of c-myc mRNA in both uninduced and 1,25(OH)-2D-3-induced HL60 cells to gt 60 min, indicating a translational requirement for the destabilization process. Additionally, the c-myc mRNA instability induced by 1,25(OH)-2D-3 in HL-60 appears to be a specific result of this agent, as indicated by the inability of other monocytic and granulocytic differentiation inducing agents to destabilize c-myc mRNA.

L4 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN

AN 1992:230257 CAPLUS

DN 116:230257

OREF 116:38859a,38862a

TI What determines the instability of c-myc proto-oncogene mRNA?

AU Laird-Offringa, Ite A.

CS Dep. Microbiol. Mol. Genet., Harvard Med. Sch., Boston, MA, 02115, USA

SO BioEssays (1992), 14(2), 119-24

CODEN: BIOEEJ; ISSN: 0265-9247

DT Journal; General Review

LA English

AB A review with 38 refs. on the mechanism of degradation of c-myc mRNA, and its similarity with c-fos mRNA decay. The c-myc proto-oncogene is believed to be involved in the regulation of cell growth and differentiation. Deregulation of this gene, resulting in an inappropriate increase of gene product, can contribute to cancer formation. One of the ways in which the expression of the c-myc gene can be deregulated is by the stabilization of the labile c-myc mRNA. The rapid degradation of the c-myc transcripts appears to be mediated by at least 2 distinct regions in the mRNA. One lies in the 3' untranslated region, and presumably consists of (A+U)-rich sequences. The other lies in the C-terminal part of the coding region and colocalizes with sequences encoding protein-dimerization motifs. The exact mechanism by which the destabilizing elements function is not yet clear. Shortening of the poly(A) tail of the c-myc message appears to precede degradation of the transcript. When translation is blocked, this shortening is slowed down and the mRNA is stabilized. This suggests that deadenylation is required before degradation of the mRNA body can take place.

L4 ANSWER 12 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson  
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DUPLICATE 7

AN 1991:340854 BIOSIS

DN PREV199192040229; BA92:40229

TI RAPID C-MYC MESSENGER RNA DEGRADATION DOES NOT REQUIRE  
A PLUS U-RICH SEQUENCES OR COMPLETE TRANSLATION OF THE MESSENGER  
RNA.

AU LAIRD-OFFRINGA I A [Reprint author]; ELFFERICH P; VAN DER EB A J  
CS DEP MICROBIOL MOL GENET, HARVARD MED SCH, 200 LONGWOOD AVE,  
BOSTON, MASS  
02115, USA

SO Nucleic Acids Research, (1991) Vol. 19, No. 9, pp. 2387-2394.  
CODEN: NARHAD. ISSN: 0305-1048.

DT Article

FS BA

LA ENGLISH

ED Entered STN: 31 Jul 1991

Last Updated on STN: 1 Aug 1991

AB The c-myc proto-oncogene encodes a highly unstable  
mRNA. Stabilized, truncated myc transcripts have been found in  
several

human and murine tumors of hematopoietic origin. Recently, two  
tumors

expressing 3' truncated c-myc mRNAs that were five  
times more stable than normal myc transcripts, were described.

We have

tried to determine the cause of the increased stability of the 3'  
truncated myc transcripts by studying the half-life of mutated c  
-myc mRNAs. The c-myc 3' untranslated  
region has been shown to contain sequences that confer mRNA  
instability. Possible candidates for such sequences are two (A +  
U)-rich regions in the 3' end of the c-myc RNA that  
resemble RNA destabilizing elements present in the c-fos and

GMCSF mRNAs.

We show that deletions in the (A + U)-rich regions do not  
stabilize

c-myc messengers, and that hybrid mRNAs containing SV40  
sequences at their 3' ends and terminating at an SV40

polyadenylation

signal decay as quickly as normal c-myc transcripts.

Our results indicate that neither the loss of (A + U)-rich  
sequences nor

the mere addition of non-myc sequences to the 3' end of the mRNA  
lead to

stabilization. We also show that rapid degradation of c-  
myc mRNA does not require complete translation of the coding  
sequences.

L4 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN

AN 1991:56810 CAPLUS

DN 114:56810  
OREF 114:9641a,9644a  
TI Cis-acting determinants required for c-myc  
mRNA instability and their mechanistic implications  
AU Mango, Susan Elizabeth  
CS Princeton Univ., Princeton, NJ, USA  
SO (1990) 133 pp. Avail.: Univ. Microfilms Int.; Order No.  
DA9027580  
From: Diss. Abstr. Int. B 1990, 51(5), 2209-10  
DT Dissertation  
LA English  
AB Unavailable

L4 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN

AN 1989:52215 CAPLUS

DN 110:52215

OREF 110:8517a,8520a

TI Activation of the transforming potential of the human fos  
proto-oncogene  
requires message stabilization and results in increased amounts  
of  
partially modified fos protein

AU Lee, William M. F.; Lin, Chin; Curran, Tom

CS Cancer Res. Inst., Univ. California, San Francisco, CA, 94143,  
USA

SO Molecular and Cellular Biology (1988), 8(12), 5521-7  
CODEN: MCEBD4; ISSN: 0270-7306

DT Journal

LA English

AB The requirements for activation of the transformation potential  
of the  
human c-fos proto-oncogene were investigated. Recombinant  
plasmids containing  
the Moloney murine leukemia virus long terminal repeat directing  
transcription of the c-fos coding region and either the  
authentic c-fos 3'  
untranslated region (UTR) or the 3' UTR from human c-myc  
were inefficient at inducing transformation. In contrast, a  
recombinant  
that substituted most of the c-fos 3' UTR with the 3' portion of  
the  
simian virus 40 T-antigen gene transformed cells well. This  
difference in  
transformation efficiency appeared to be due to significantly  
higher  
levels of fos mRNA and protein expressed from the transforming  
recombinant. This, in turn, was due to the much greater  
stability of its  
mRNA compared with those from the poorly transforming  
recombinants containing  
the c-fos or c-myc 3' UTR. Thus, the 3' UTR of the  
human c-fos mRNA is responsible for its rapid degradation and  
limits the



steady-state levels of transcript and protein. Cells transformed by the activated human c-fos plasmids contained increased amts. of partially modified c-fos protein (c-Fos). This form of c-fos turned over much more rapidly than the highly modified form of c-fos induced by serum stimulation.

L4 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN

AN 1985:22195 CAPLUS

DN 102:22195

OREF 102:3645a,3648a

TI Extreme instability of myc mRNA in normal and transformed human cells

AU Dani, C.; Blanchard, J. M.; Piechaczyk, M.; El Sabouty, S.; Marty, L.;

Jeanteur, P.

CS Lab. Biol. Mol., Univ. Sci. Tech. Languedoc, Montpellier, 34060, Fr.

SO Proceedings of the National Academy of Sciences of the United States of

America (1984), 81(22), 7046-50

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB To address the possibility that the expression of the myc gene might be

regulated at a post-transcriptional level, the half-life of myc mRNA in

various cells was investigated. The survey included normal human embryonic fibroblasts as well as transformed human cells of various

origins: cervix carcinoma (HeLa), breast carcinoma (MCF7), Burkitt

lymphoma (Daudi), and promyelocytic leukemia (HL60). All these cells

revealed an extreme instability of myc mRNA (half-life, .apprx.10 min), suggesting that the control of myc mRNA

degradation might be a general means (although not necessarily exclusive) of

regulating both the level and the timing of myc gene expression. Inhibition of protein synthesis resulted in a dramatic stabilization of

myc mRNA in HeLa, MCF7, and HL60 cells, suggesting that the controlling

element might itself be, at least in these cells, a protein of rapid

turnover. This finding opens the way to studying the mechanism of myc

mRNA inactivation in these different cell types. However, protein

synthesis inhibition had no effect on myc mRNA  
instability in other transformed (Daudi) cells lines as well as  
normal embryonic human fibroblasts. These different types of  
behavior  
suggest that the post-transcriptional control of myc gene  
expression might  
involve multiple factors that would be differently affected in  
various  
cell types.

=> FIL STNGUIDE		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	51.57	51.78
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	-4.00	
-4.00		

FILE 'STNGUIDE' ENTERED AT 19:14:15 ON 04 SEP 2008  
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FILE CONTAINS CURRENT INFORMATION.  
LAST RELOADED: Aug 29, 2008 (20080829/UP).

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---Logging off of STN---

=>

Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.18	51.96
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	
-4.00		

STN INTERNATIONAL LOGOFF AT 19:16:04 ON 04 SEP 2008

## WEST Search History for Application 10814634

Creation Date: 2008090419:37

Query	DB	Op.	Plur.	Thes.	Date
instab\$ near3 mRNA	PGPB, USPT, JPAB, DWPI	ADJ			09-04-2008
(instab\$ near3 mRNA ) and CRD	PGPB, USPT, JPAB, DWPI	ADJ			09-04-2008
(instab\$ near3 mRNA ) same rapa\$	PGPB, USPT, JPAB, DWPI	ADJ			09-04-2008
(instab\$ near3 mRNA ) and rapa\$	PGPB, USPT, JPAB, DWPI	ADJ			09-04-2008
(instab\$ near3 mRNA and rapa\$ ) and @pd > 20080130	PGPB, USPT, JPAB, DWPI	ADJ			09-04-2008